Serial No. 10/627,132
Amendment Dated June 10, 2005
Reply to Office Action of March 11, 2005

APPENDIX A

Alignment of maize CesA proteins The common motifs (D, D, and QXXRW) are marked with an asterisk on top. These motifs are found in all processive beta-glycosyltransferases (Saxena et al., 1995, Multidomain architecture of beta-glycosyltransferases: implications for mechanism of action, J. Bacteriol. 177:1419-1424). Aside from these motifs, many other domains are completely conserved among dicot (Arabidopsis) and monocot (maize) CesA proteins.

```
                                 1                                                 50
ZmCesA9      (1)  ------------------------------MEGDADGVKSGRRGGGQVCQICGDG
ZmCesA8      (1)  ---MEASAGLVAGSHNRNELVVIRRDRESGAAGGGAARRAEAPCQICGDE
ZmCesA7      (1)  ---MEASAGLVAGSHNRNELVVIRRDGDP--GPKPPREQNGQVCQICGDD
ZmCesA6      (1)  ------------------------------MDQRNGQVCQICGDD
ZmCesA5      (1)  -----------------------------MDGGDATNSGKHVAGQVCQICGDG
ZmCesA4      (1)  --------------------------MEGDADGVKSGRRGGGQVCQICGDG
ZmCesA3      (1)  -------------------------------------------------
ZmCesA2      (1)  ---MAANKGMVAGSHNRNEFVMIRHDGDAPVPAKPTKSANGQVCQICGDT
SEQIDNO.30   (1)  ---MEASAGLVAGSHNRNELVLIRGHEDP----KPLRALSGQVCEICGDE
ZmCesA12     (1)  ------------------------------MMESAAAQSCAACGDD
ZmCesA11     (1)  ----------------------------MDAGSVTGGLAAGSHMRDELHVMRARAEEP---NAKVRSADVKTCRVCADE
ZmCesA10     (1)  MDAGSVTGGLAAGSHMRDELHVMRARAEEP---NAKVRSADVKTCRVCADE
ZmCesA1      (1)  ---MAANKGMVAGSHNRNEFVMIRHDGDVPGSAKPTKSANGQVCQICGDS
Consensus    (1)                                 D          R    GQVCQICGD
                                 51                                               100
ZmCesA9     (26)  VGTTAEGDVFTACDVCGFPVCRPCYEYERKDGTQACPQCKNKYKRHKGSP
ZmCesA8     (48)  VGVGFDGEPFVACNECAFPVCRACYEYRRREGSQACPQCRTRYKRLKGCP
ZmCesA7     (46)  VGLAPGGDPFVACNECAFPVCRDCYEYERRECTQNCPQCKTRYKRLKGCQ
ZmCesA6     (16)  VGRNPDGEPFVACNECAFPICRDCYEYERREGTQNCPQCKTRFKRPKGCA
ZmCesA5     (25)  VGTAADGDLFTACDVCGFPVCRPCYEYERKDCTQACPQCKTKYKRHKGSP
ZmCesA4     (26)  VGTTAEGDVFAACDVCGFPVCRPCYEYERKDGTQACPQCKTKYKRHKGSP
ZmCesA3      (1)  -------------------------------------------------
ZmCesA2     (48)  VGVSATGDVFVACNECAFPVCRPCYEYERKEGNQCCPQCKTRYKRQKGSP
SeqIdNo.30  (44)  VGLTVDGDLFVACNECGFPVCRPCYRYERREGTQNCPQCKTRYKRLKGSP
ZmCesA12     (1)  -------------------------------------------------
ZmCesA11    (17)  AR--------AACRACSYALCRACLDEDAAEGRTTCARCGGDYAAINPAR
ZmCesA10    (48)  VGTREDGQPFVACAECGFPVCRPCYEYERSEGTQCCPQCNTRYKRQKCCP
ZmCesA1     (48)  VGVSATGDVPVACNECAFPVCRPCYEYERKEGNQCCPQCKTRYKRQKGSP
Consensus   (51)  VG    DGD FVAC ECAFPVCRPCYEYERKEGTQ CPQCKTRYKR KGSP
                                 101                                              150
ZmCesA9     (76)  AIRGEE-GDDTDADDASDFNYPASGND-------DQKQKIADRMRSWRMNA
ZmCesA8     (98)  RVAGDE-EEDGVDDLEGEFCLQDGAAHE-----DDPQYVAESMIRAQMSY
ZmCesA7     (96)  RVTGDE-EEDGVDDLBNEFNWDG----------HDSQSVAESMLYGHMSY
ZmCesA6     (66)  RVPGDE-EEDGVDDLENEFNWSDK---------HDSQYLAESMLHAHMSY
ZmCesA5     (75)  PVHGEE-NEDVDADDVSDYNYQASGNQ------DQKQKIAERMLTWRTNS
ZmCesA4     (76)  AIRGEE-GDDTDAD--SDFNYLASGNE------DQKQKIADRMRSWRMNV
ZmCesA3      (1)  -------------------------------------------------
ZmCesA2     (98)  RVHGDD-EEDVDDLDNEFNYKQGNGK-------GPEWQLQGDDADLSSSA
SeqIdNo.30  (94)  RVAGDD-DEEDIDDLEHEFNIDDENQQRQLEGNMQNSQITEAMLHGRMSY
ZmCesA12     (1)  --------------------------------MQNSQITEAMLHGRMSY
ZmCesA11    (59)  ASEGTEAKEEVVENHHTAGGLRERVTMGSHLNDRQDEVSHARTMSSLSGI
ZmCesA10    (98)  RVEGDEEEGPEMDDFEDEFPAKS-----------PKKPHEPVAFDVYSE
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Serial No. 10/627,132
Amendment Dated June 10, 2005
Reply to Office Action of March 11, 2005

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ZmCesA1      (98)  RVHGDE-DEEDVDDLDNEFNYKQGSGK------GPEWQLQGDDADLSSSA
Consensus   (101)  RV GDE EED VDD E EFNY               I E ML      MS

                   151                                            200
ZmCesA9     (119)  GGSGDVGRPKYDSGEIGLTKYDSGEIPRGYIPSVTNSQISGEIPGASPDH
ZmCesA8     (142)  GRG---GDAHPGFSPVPNVPLLTNGQMVDDIPPEQHALVPSYMSGGGGCG
ZmCesA7     (135)  GRGGDPNGAPQAFQLNPNVPLLTNGQMVDDIPPEQHALVPSFMGGGG---
ZmCesA6     (106)  GRGADLDGVPQPFHPIPNVPLLTNGQMVDDIPPDQHALVPSFVGGGG---
ZmCesA5     (118)  RGS-DIGLAKYDSGEIGHGKYDSGEIPRGYIPSLTHSQISGEIPGASPDH
ZmCesA4     (117)  GGSCDVGRPKYDSGEIGLTKYDSGEIPRGYIPSVTNSQISGEIPGASPDH
ZmCesA3       (1)  -------------------------------------------------
ZmCesA2     (141)  RHDPHHRIPRLTSGQQ----------------IS-----GEIPDASPDR
SeqIdNo.30  (143)  GRG---PDDGDGNNTPQIPPYIITGSRSVPVSGEFPITNGYCHGEVSSSLH
ZmCesA12     (18)  GRG---PDDGDGNNTPQIPPIITGSRSVPVSGEFPITNGYGHGEVSSSLH
ZmCesA11    (109)  GSELN--------------------------------------------
ZmCesA10    (136)  NGE----------------------------------------------
ZmCesA1     (141)  RHEPHHRIPRLTSGQQ----------------IS-----GEIPDASPDR
Consensus   (151)  G                       T              G I  AS
                   201                                            250
ZmCesA9     (169)  HMMSPTGNIGRRAPFPYMNHSSNPSRE-FSGSVGNVAWKERVDGWKMKQD
ZmCesA8     (189)  KRIHPLPFA--DPNLPVQPRSMDPSKDLAAYGYGSVAWKERMEGWKQKQE
ZmCesA7     (182)  KRIHPLPYA--DPSLPVQPRSMDPSKDLAAYGYGSVAWKERMENWKQRQE
ZmCesA6     (153)  KRIHPLPYA--DPNLPVQPRSMDPSKDLAAYGYGSVAWKERMESWKQKQE
ZmCesA5     (167)  MMSPVGNIGRRGHQFPYVNHSPNPSRE-FSGSLGNVAWKERVDGWKMK-D
ZmCesA4     (167)  HMMSPTGNIGKRAPFPYVNHSPNPSRE-PSGSIGNVAWKERVDGWKMKQD
ZmCesA3       (1)  -------------------------------------------------
ZmCesA2     (169)  HSIRSPTSSYVDPSVPVPVRIVDPSKDLNSYGLNSVDWKERVESWRVKQD
SeqIdNo.30  (190)  KRIHPYPVS--EPGSAKWDE------------KKEVSWKERMDDWKSKQG
ZmCesA12     (65)  KRIHPYPVS--EPGSAKWDE------------KKEVSWKERMDDWKSKQG
ZmCesA11    (114)  --------------DE--SGK---------------PIWKNRVESWKEKKN
ZmCesA10    (139)  -HPAQKWRTGGQTLSSFTCSVAGKDLEAEREMEGSMEWKDRIDKWKTKQE
ZmCesA1     (169)  HSIRSPTSSYVDPSVPVPVRIVDPSKDLNSYGLNSVDWKERVESWRVKQD
Consensus   (201)     I P   S  DP  P        PSKD  S   G VAWKERVD WK KQD
                   251                                            300
ZmCesA9     (218)  KGTIPMTNGTSIAPSEGRGVGDIDASTDYNMEDALLNDETRQPLSRKVPL
ZmCesA8     (237)  RLQHVRS-----------EGGG--DWDGDDADLPLMDEARQQLSRKIPL
ZmCesA7     (230)  RMHQTGN-----------DGG---GDDGDDADLPLMDEARQPLSRKIPL
ZmCesA6     (201)  RMHQTRN-----------DGG---GDDGDDADLPLMDEARQPLSRKIPL
ZmCesA5     (215)  KGAIPMTNGTSIAPSEGRGVADIDASTDYNMEDALLNDETRQPLSRKVPT
ZmCesA4     (216)  KGTIPMTNGTSIAPSEGRGVGDIDASTDYNMEDALLNDETRQPLSRKVPL
ZmCesA3       (1)  --------------------------------------PLSRIVPI
ZmCesA2     (219)  KNMLQVTNKYPEARG----DMEGTGSNGE---DMQMVDDARLPLSRIVPI
SeqIdNo.30  (226)  --ILG--------------GGA--DPEDMDADVALNDEARQPLSRKVSI
ZmCesA12    (101)  --ILG--------------GGA--DPEDMDADVALNDEARQPLSRKVSI
ZmCesA11    (134)  EKKASAKKTAAKAQP----P--P---VEEQIMDEKDETDAYEPLSRVIPI
ZmCesA10    (188)  K-RGKLN-----------HDDSDDDDKNEDEYMLLAEARQPLWRKVPI
ZmCesA1     (219)  KNMMQVTNKYPEARGG---DMEGTGSNGE---XMQMVDDARLPLSRIVPI
Consensus   (251)  K  I              G       D    DL LMDEARQPLSRKVPI
                   301                                            350
ZmCesA9     (268)  PSSRINPYRMVIVLRLIVLSIFLHYRITNPVRNAYPLWLLSVICEIWFAL
ZmCesA8     (273)  SSSRINPYRMIIVIRLVVLGFFFHYRVMHPAKDAFALWLISVICEIWFAM
ZmCesA7     (265)  PSSQINPYRMIIIIRLVVLGFFFHYRVMHPVNDAFALWLISVICEIWFAM
ZmCesA6     (236)  PSSQINPYRMILIIRLVVLCFFFHYRVMHPVPDAFALWLISVICEIWFAM
ZmCesA5     (265)  PSSRINPYRMVIVLRLIAVLCIFLRYRITHPVNNAYPLWLLSVICEIWFAL
ZmCesA4     (266)  PSSRINPYRMVIVLRLIVLSIFLHYRITNPVRNAYPLWLLSVICEIWFAL
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Serial No. 10/627,132
Amendment Dated June 10, 2005
Reply to Office Action of March 11, 2005

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ZmCesA3     (9)    SPNELNLYRIVIVLRLIILCFFFQYFITHPVEDAYGLWLVSVICEVWFAL
ZmCesA2     (262)  SSNQLNLYRIVIILRLIILCFFFQYRISHPVRNAYGLWLVSVICEIWFAI
SeqIdNo.30  (257)  ASSKVNPYRMVIVVRDVVLAFFLRYRILHPVPDAIGLWLVSIICEIWFAY
ZmCesA12    (132)  ASSKVNPYRMVIVVRLVVIAFFLRYRILHPVPDAIGLWLVSTICEIWFQF
ZmCesA11    (175)  SKNKLTPYRAVIIMRLIVLGLFFHYRITNPVNSAFGLWMTSVICEIWFQF
ZmCesA10    (225)  PSSMINPYRIVIVLRLVVVCFFLKFRITTPATUAVPLWLASVICELWFAF
ZmCesA1     (263)  SSNQLNLYRVVIILRLIILCFFFQYRVSHPVRDAYGLWLVSVICEVWFAL
Consensus   (301)  SSSRINPYRMVIVLRLIVL FFF YRITHPV DAYGLWLVSVICEIWPAL
                   351                                              400
ZmCesA9     (318)  SWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPMKE
ZmCesA8     (323)  SWILDQFPKWLEIERETYLDRLSLRFDKEGQPSQLAPIDFVSTVDPTKE
ZmCesA7     (315)  SWILDQFPKWFPIERETYLDRLSLRFDKEGQPSQLAPIDFFVSTVDPLKE
ZmCesA6     (286)  SWILDQFPKWFPIERETYLDRLSLRFDKFGHPSQLAPVDFFVSTVDPLKE
ZmCesA5     (315)  SWILDQFPKWSPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPMKE
ZmCesA4     (316)  SWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAPIDVFVSTVDPLKE
ZmCesA3     (59)   SWLLDQFPKWYPINRETYLDRLALRYDREGEPSQLAPIDVFVSTVDPLKE
ZmCesA2     (312)  SWILDQFPKWFPIDRETYLDRLSLRYEREGEPSLLSAVDLFVSTVDPLKE
SeqIdNo.30  (307)  SWILDQFPKWFIDRETYLDRLSLRYEREGEPSLLSAVDLFVSTVDPLKE
ZmCesA12    (182)  SWILDQFPKWFEIDRETYLDRLSLRYEREGEPSLLSAVDLFVSTVDPLKE
ZmCesA11    (225)  SWILDQFPKWYPINRETYVDRLIARYG-DGEESGLAPVDFFVSTVDPLKE
ZmCesA10    (275)  SWILDQLPKWAPVTRETYLDRLALRYDREGEACRLSPIDFFVSTVDPLKE
ZmCesA1     (313)  SWLLDQFPKWYPINRETYLDRLALRYDREGEPSQLAPIDVFVSTVDPLKE
Consensus   (351)  SWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAPVDIFVSTVDPLKE
                   401                                 *           450
ZmCesA9     (368)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFDALAETSEFARKWV
ZmCesA8     (373)  PPLVTTNTVLSILSVDYPVDKVSCYVSDDGAAMLTFEALSETSEFAKKWV
ZmCesA7     (365)  PPLVTTNTVLSILSVDYPVDKVSCYVSDDGAAMLTFEALSETSEFAKKWV
ZmCesA6     (336)  PPLVTANTVLSILSVDYPVDKVSCYVSDDGAAMLTFEALSETSEFARKWV
ZmCesA5     (365)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFDALSETSEFARKWV
ZmCesA4     (366)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFDALAETSEFARKWV
ZmCesA3     (109)  PPLITGNTVLSILAVDYPVDKVSCYVSDDGSAMLTFEALSETAEFARKWV
ZmCesA2     (362)  PPLITANTVLSILAVDYPVDKVSCYVSDDGSAMLTFESLSETAEFARKWV
SeqIdNo.30  (357)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFESLSETAEFARKWV
ZmCesA12    (232)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFESLAETAEYARKWV
ZmCesA11    (274)  PPLITANTVLSILAVDYPVEKISCYVSDDGASMLLFDALSETAEFARKWV
ZmCesA10    (325)  PPLITANTVLSILAVDYPVDKVSCYVSDDGSAMLTFESLSETAEFARKWV
ZmCesA1     (363)  PPLITANTVLSILSVDYPVDKVSCYVSDDGAAMLTFESLSETAEFARKWV
Consensus   (401)  PPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFEALSETAEFARKWV
                   451                                             500
ZmCesA9     (418)  PFVKKYNIEPRAPEWYFSQKIDYLKDKVHPSFVKDRRAMKREYEEFKIRV
ZmCesA8     (423)  PFSKKENIEPRAPEWYFQQKIDYLKDKVAASFVRERRAMKREYEEFKVRI
ZmCesA7     (415)  PFCKRYNIEPRAPEWYFQQKIDYLKDKVAANFVRERRAMKREYEEFKVRI
ZmCesA6     (386)  PFCKRYSIEPRAPEWYROQKIDYLRDKVAPNEVRERRAMKREYEEFKVRI
ZmCesA5     (415)  PFVKKYNIEPXAPEWYFAQKIDYLKDKVHPSFVKDRRAMKREYEEFKVRV
ZmCesA4     (416)  PFVKKYNIEPRAPEWYFSQKIDYLKDKIQPSFVKERRAMKRECEEFKVRI
ZmCesA3     (159)  PFCKKHNIEPRAPEFVFAQKIDYLKDKIQPSFVKERRAMKREYEEFKIRI
ZmCesA2     (412)  PFCKKHNIEPRAPEFYFAQKIDYLKDKIQPSFVKERRAMKREYEEFKVRI
SeqIdNo.30  (407)  PFCKKFGIEPRAPEFYFSLKVDYLKDKVQPTFVQERRAMKREYEEFKVRI
ZmCesA12    (282)  PFCKKFGIEPRAPEFYFSLKVDYLKDKVQPTFVQERRAMKREYEEFKVRI
ZmCesA11    (324)  PFCKKYAIEPRAPEFYFSQKIDYLKDKIHPSFVKERRAMKRDYEEYKVRI
ZmCesA10    (375)  PFCKKFAVEPRAPEFYFSQKIDYLKDKVQPTFVKERRAMKREYEEFKVRI
ZmCesA1     (413)  PFCKKHNIEPRAPEFYFAQKIDYLKDKIQPSFVKERRAMKREYEEFKVRI
Consensus   (451)  PFCKKYNIEPRAPEFYFSQKIDYLKDKVQPSFVKERRAMKREYEEFKVRI
                   501                                             550
ZmCesA9     (468)  NGLVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGN
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Page 21 of 25

PAGE 23/27 * RCVD AT 6/10/2005 9:31:42 AM [Eastern Daylight Time] * SVR:USPTO-EFXRF-1/1 * DNIS:8729306 * CSID:515 334 6883 * DURATION (mm-ss):11-54

Serial No. 10/627,132
Amendment Dated June 10, 2005
Reply to Office Action of March 11, 2005

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ZmCesA8      (473)  NALVAKAQKVPEEGWTMQDGSPWPGNNVRDHPGMIQVFEGQSGGRDVEGN
ZmCesA7      (465)  NALVAKAQKVPEEGWTMQDGTPWPCNNVRDHPGMIQVFLGQSGGLDCEGN
ZmCesA6      (436)  NGLVAKAQKVPEEGWTMQDGTPWPGNNVRDHPGMIQVFLGQSGGCLDVEGN
ZmCesA5      (465)  NGLVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGN
ZmCesA4      (466)  NGLVAKAQKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTDGN
ZmCesA3      (209)  DALVAKAQKIPEEGWTMADGTPWPGNNPRDHPGMIQVFLGHSGGLDTDGN
ZmCesA2      (462)  NALVAKAQKVPEEGNTMADGTAWPGNNTRDHPGMIQVFLGHSGCHDTEGN
SeqIdNo.30   (457)  NALVAKAMKVPAEGWIMKDGTPWPGNNTRDHPGMIQVFLGHSGGHDTEGN
ZmCesA12     (332)  NADVAKBMKVPAEGWIMKEGTPWPGNNTRDHPGMIQVFLGETGARDFDGN
ZmCesA11     (374)  NALVAKAQKTPDEGWIMQDGTPWPGNNPRDHPGMIQVFLGETGARDFDGN
ZmCesA10     (425)  NALVAKAQKKPEEGWVMQDGTPWPGNNTRDHBGMIQVYLGNQCALDVEGH
ZmCesA1      (463)  NALVAKAQKVPEEGWTMADGTAWPGNNPRDHPGMIQVFLGHSGGLDTDGN
Consensus    (501)  NALVAKAQKVPEEGWIMQDGTPWPGNN RDHPGMIQVFLGHSGGLDTEGN
                                                                      *600
                    551
ZmCesA9      (518)  ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYI
ZmCesA8      (523)  ELPRLVYVSREKRPCYNHHKKAGAMNALVRVSAVLTNAPYLLNLDCDHYI
ZmCesA7      (515)  ELPRLVYVSREKRPGYNHHKKAGAMNALVRVSAVLTNAPYLLNLDCDHYI
ZmCesA6      (486)  ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYI
ZmCesA5      (515)  ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYI
ZmCesA4      (516)  ESPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYI
ZmCesA3      (259)  ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYF
ZmCesA2      (512)  ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYF
SeqIdNo.30   (507)  ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNAPFMLNLDCDHYI
ZmCesA12     (382)  ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNAPFMLNLDCDHYI
ZmCesA11     (424)  ELPRLVYVSREKRPGYQHHKKAGAMNALVRVSAVLTNAPYILNLDCDHYV
ZmCesA10     (475)  ELPRLVYVSREKRPGYNHHKKAGAMNALVRVSAVLTNAPFILNLDCDHYV
ZmCesA1      (513)  ELPRLVYVSREKRPGFQHHKKAGAMNALIRVSAVLTNGAYLLNVDCDHYF
Consensus    (551)  ELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNA YLLNLDCDHYI
                    601                                               650
ZmCesA9      (568)  NNSKALREAMCFLMDPNLGRSVCYVQFPQRFDGIDRNDRYANPNTVFFDI
ZmCesA8      (573)  NNSKALKEAMCFMMDPLVGKKVCYVQFPQRFDGIDRNDRYANRNVVFFDI
ZmCesA7      (565)  NNSKALKEAMCFMMDPLLGKKVCYVQFPQRFDGIDRHDRYANRNVVFFDI
ZmCesA6      (536)  NNSKALKEAMCFMMDPLLGKKVCYVQFPQRFDGIDRHDRYANRNVVFFDI
ZmCesA5      (565)  NNSKALREAMCFLMDPNLGRNVCYVQFPQRFDGIDRNDRYANRNTVFFDI
ZmCesA4      (566)  NNSKALREAMCFLMDPNLGRSVCYVQFPQRFDGIDLHDRYANRNIVFFDI
ZmCesA3      (309)  NSSKALREAMCFMMDPALGRKTCYVQFPQRFDGIDLHDRYANRNIVFFDI
ZmCesA2      (562)  NSSKALREAMCFMMDPALGRKTCYVQFPQRFDGIDLHDRYANRNIVFFDI
SeqIdNo.30   (557)  NNSKAIREAMCFLMDPQVGRKVCYVQFPQRFDGIDVHDRYANRNTVFFDI
ZmCesA12     (432)  NNSKAIREAMCFLMDPQVGRKVCYVQFPQRFDGIDVHDRYANRNTVFFDI
ZmCesA11     (474)  NNSKAVREAMCFMMDPTVGRDVCYVQFPQREDGIDRSDRYANRNVVFFDV
ZmCesA10     (525)  NNSKAVREAMCFIMDPQLGKKLCYVQFPQREDGIDRHDRYANRNVVFFDI
ZmCesA1      (563)  NSSKALREAMCFMMDPALGRKTCYVQFPQRFDGIDLHDRYANRNIVFFDI
Consensus    (601)  NNSKALREAMCFMMDP LGRKVCYVQFPQRFDGIDRHDRYANRNVVFFDI
                    651                                               700
ZmCesA9      (618)  NLRGLDGIQGPVYVGTGCVFNRTALYGYEPPIKQKKGG--------FLS
ZmCesA8      (623)  NMKGLDGIQGPIYVGTGCVFRRQALYGYDAPKTKKPPSRTCNCWPKWCSS
ZmCesA7      (615)  NMKGLDGIQGPIYVGTGCVFRRQALYGYDAPKTKKPPSRTCNCWPKWCIC
ZmCesA6      (586)  NMKGLDGIQGPIYVGTGCVFRRQALYGYDAPKTKKPPSRTCNCWPKWCIC
ZmCesA5      (615)  NLRGLDGIQGPVYVGTGCVFNRTALYGYEPPVKKKKPG---------PFS
ZmCesA4      (616)  NLRGLDGIQGPVYVGTGCVFNRTALYGYEPPIKQKKGG--------FLS
ZmCesA3      (359)  NMKGLDGIQGPVYVGTGCCFNRQALYGYDPVLTEADLEP------NIILK
ZmCesA2      (612)  NMKGLDGIQGPVYVGTGCCFNRQALYGYDPVLTEADLEP------NIVVK
SeqIdNo.30   (607)  NMKGLDGIQGPVYVGTGCVFRRQALYGYNPPKGPKRPK------MVTCDC
ZmCesA12     (482)  NMKGLDGIQGPVYVGTGCVFRRQALYGYNPPKCPKRPK------MVTCDC
ZmCesA11     (524)  NMKGLDGIQGPVYVGTGCCFNRQALYGYGPPSLPALPKS------SICSW
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Serial No. 10/627,132
Amendment Dated June 10, 2005
Reply to Office Action of March 11, 2005

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ZmCesA10    (575)  NMKGLDGIQGPVYVGTGCVFNRQALYGYDPPRPEKRPKMTCDCWPSWCCC
ZmCesA1     (613)  NMKGLDGIQGPVYVGTGCCFNRQALYGYDPVLTEADLEP------NIVIK
Consensus   (651)  NMKGLDGIQGPVYVGTGCVFNRQALYGYDPP     K P          CI
                   701                                                   750

ZmCesA9     (659)  SLCGGRK----------------------------------KGSKSKKGSDKKKSQK
ZmCesA8     (673)  CCCSRNK----------------------------------NKKKTTKPKTEKKKRLFFK
ZmCesA7     (665)  CCCFGNR----------------------------------KQKKTTKPKTEKKKLLFFK
ZmCesA6     (636)  CCCFGNRKTK-------------------------------KKTKTSKPKFEKIKKLFKK
ZmCesA5     (656)  SLCGGRK----------------------------------KTSKSKKSSEKKKSHR
ZmCesA4     (657)  SLCGGRK----------------------------------KASKSKKGSDKKKSQK
ZmCesA3     (403)  SCCGGRK----------------------------------KKDKSYIDS-KNRDMK
ZmCesA2     (656)  SCCGRRK----------------------------------RKNKSYMDS-QSRIMK
SeqIdNo.30  (651)  CPCFCRK----------------------------------KRKHAKDGLPEG------
ZmCesA12    (526)  CPCFGRK----------------------------------KRKHAKDGLPEG------
ZmCesA11    (568)  CCCCCPK----------------------------------KK-VERSEREINRDSR
ZmCesA10    (625)  CCCFGGGKRGKARKDKKGDGGEEPRRGLLGFYRKRSKKDKLGGGSVAGSK
ZmCesA1     (657)  SCCGRRK----------------------------------KKNKSYMDS-QSRIMK
Consensus   (701)  CCC GRK                                  K  KKE  KR   K
                   751                                                   800

ZmCesA9     (682)  HV----DSSVPVFNLFDIEEGVECAGFDDEKSLLMSQMSLEKRFGQSAAF
ZmCesA8     (699)  KA----ENPSPAYALGEIDEGAPG--ADIEKAGIVNQQKLEKKFGQSSVF
ZmCesA7     (691)  KE----ENQSPAYALGEIDEAAPG--AENEKAGIVNQQKLEKKFGQSSVF
ZmCesA6     (665)  KE-----NQAPAYALGEIDEAAPG--AENEKASIVNQQKLEKKFGQSSVF
ZmCesA5     (679)  HA----DSSVPVFNLEDIEEGIEGSQFDDEKSLLMSQMSLEKRFGQSAAF
ZmCesA4     (680)  HV----DSSVPVFNLEDIEEGVEGAGFDDEKSLLMSQMSLEKRFGQSAAF
ZmCesA3     (425)  RT----ESSAPIFNMEDIEEGFEG--YEDERSLLMSQKSLEKRFGQSPIF
ZmCesA2     (678)  RT----ESSAPIFNMEDIEEGIEG--YEDERSVLMSORKLEKRFGQSPIF
SeqIdNo.30  (670)  ------------------TADMG--VDSDKEMLMSHMNFEKRFGQSAAF
ZmCesA12    (545)  ------------------TADMG--VDSDKEMLMSHMNFEKRFGQSAAF
ZmCesA11    (590)  RE----DLESAIFNLREIDNYDEY------ERSMLISQMSFEKSFGLSSVF
ZmCesA10    (675)  KGGGLYKKHQRAFELEEIEEGLEG-YDELERSSLMSQKSPEKRFGQSPVF
ZmCesA1     (679)  RT----ESSAPIFNMEDIEEGIEG--YEDERSVLMSQRKLEKRFGQSPIF
Consensus   (751)  K        E   APIFNLEDIEEG EG     D EKSLLMSQ  LEKRFCQSSVF
                   801                                                   850

ZmCesA9     (728)  VASTLMEYGGVPQ--SATRESLLKEAIHVISCGYEDKIEWGTEIGWIYGS
ZmCesA8     (743)  VASTLDENGGTLK--SASPASLLKEAIHVISCGYEDKTDWGKEIGWIYGS
ZmCesA7     (735)  VTSLLLENGGTLK--SASPASLLKEAIHVISCGYEDKTDWGKDIGWIYGS
ZmCesA6     (708)  VASLLLENGGTLK--SASPASLLKEAIHVISCGYEDKTGWGKDIGWIYGS
ZmCesA5     (725)  VASTLMEYGGVPQ--SATRESLLKEAIHVISCGYEDKTDWGTEIGWIYGS
ZmCesA4     (726)  VASTLMEYGGVPQ--SATRESLLKEAIHVISCGYEDKTEWGTEIGWIYGS
ZmCesA3     (469)  IASTFMTQGGIPP--STNPGSLLKEAIHVISCGYEDKTEWGKEIGWIYGS
ZmCesA2     (722)  IASTFMTQGGIPP--STNPASLLKEAIHVISCGYEDKTEWGKEIGWIYGS
SeqIdNo.30  (699)  VTSTLMEEGGVPP--SSSPAALLKEAIHVISCGYEDKTDWGLELGWIYGS
ZmCesA12    (574)  VTSTLMEEGGVPP--SSSPAALLKEAIHVISCGYEEKTEWGKEIGWIYGS
ZmCesA11    (631)  IASTLMENGGVPES--ANPSTLIKEAIHVISCGYEEKTEWGKEIGWIYGS
ZmCesA10    (724)  IASTFMTQGGIPP--STNPASLLKEAIHVISCGYEDKTEWGKEIGWIYGS
ZmCesA1     (723)  IASTFMTQGGIPP--STNPASLLKEAIHVISCGYEDKTEWGKEIGWIYGS
Consensus   (801)  VASTLMENGGVP   SASPASLLKEAIHVISCGYEDKTEWGKEIGWIYGS
                   851                                          *   *  900

ZmCesA9     (776)  VTEDILTGFKMHARGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
ZmCesA8     (791)  ITEDILTGFKMHCHGWRSIYCIPKRPAFKGSAPLNLSDRLHQVLRWALGS
ZmCesA7     (783)  VTEDILTGFKMHCHGWRSIYCIPKRVAFKGSAPLNLSDRLHQVLRWALGS
ZmCesA6     (756)  VTEDILTGFKMHCHGWRSIYCIPKRAAFKGSAPLNLSDRFHQVLRWALGS
ZmCesA5     (773)  VTEDILTGFKMHARGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
ZmCesA4     (774)  VTEDILTGFKMHARGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
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Page 23 of 25

Serial No. 10/627,132
Amendment Dated June 10, 2005
Reply to Office Action of March 11, 2005

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ZmCesA3     (517)  VTEDILTGFKMHARGWISIYCMPLRPCFKGSAPINLSDRLNQVLRWALGS
ZmCesA2     (770)  VTEDILTGFKMHARGWQSIYCMPPRPCFKGSAPINLSDRLNQVLRWALGS
SeqIdNo.30  (747)  ITEDILTGFKMHCRGWRSVYCMPKRAAFKGSAPINLSDRLNQVLRWALGS
ZmCesA12    (622)  ITEDILTGFKMHCRGWRSVYCMPKRAAFKGSAPINLSDRLHQVLRWALVS
ZmCesA11    (679)  VTEDILTGFKMHCRGWRSIYCMPVRPAFKGSAPINLSDRLHQVLRWALGS
ZmCesA10    (774)  VTEDILTGFKMHCRGWKSVYGTPTRPAFKGSAPINLSDRLNQVLRWALGS
ZmCesA1     (771)  VTEDILTGFKMHARGWQSIYCMPPRPCFKGSAPINLSDRLNQVLRWALGS
Consensus   (851)  VTEDILTGFKMHCRGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
                   901                                              950
ZmCesA9     (826)  VEILFSRHCPLWYGYGGR-LKFLERFAYINTTIYPLTSLPLLIYCILPAI
ZmCesA8     (841)  VEIFFSXHCPLWYGYGGG-LKFLERFSYINSIVYPWTSIPLLAYCTLPAI
ZmCesA7     (833)  IEIFFSNHCPLWYGYGCG-LKFLERFSYINSIVYPWTSIPLLAYCTLPAI
ZmCesA6     (806)  IEILFSNHCPLWYGYGGG-LKFLERFSYINSIVYPWTSIPLLAYCTLPAI
ZmCesA5     (823)  IEILFSRHCPIWYGYGGR-LKFLERFAYINTTIYPLTSIPLLIYCILPAI
ZmCesA4     (824)  VEILFSRHCPLWYGYGGR-LKFLERFAYINTTIYPLTSIPLLIYCILPAI
ZmCesA3     (567)  VEILLSRHCPIWYGYNGR-LKLLERLAYINTIVYPITSIPLVAYCVLPAI
ZmCesA2     (820)  VEILLSRHCPIWYGYNGR-LKLLERLAYINTIVYPITSVPLLAYCVLPAI
SeqIdNo.30  (797)  VEIFFSRHSPLLYGYKNGNLKWLERFAYINTTIYPFTSLPLLAYCTLPAV
ZmCesA12    (672)  VEIFFSRHSPLLYGYKNGNLKWLERFAYINTTIYPFTSLPLLAYCTLPAV
ZmCesA11    (729)  VEIFFSRHCPLWYGYGGGRLKWLQRLSYINTIVYPFTSLPLVAYCCLPAI
ZmCesA10    (824)  VEIFMSRHCPLRYAYGGR-LKWLERFAYTNTIVYPFTSIPLLAYCTIPAV
ZmCesA1     (821)  VEILLSRHCPIWYGYNGR-LKLLERLAYINTIVYPITSIPLIAYCVLPAI
Consensus   (901)  VEILFSRHCPLWYGYGGR LKFLERFAYINTIVYPFTSIPLLAYC LPAI
                   951                                              1000
ZmCesA9     (875)  CLLTCKFIIPEISNFASIWFISLFISIFATGILEMRWSGVCIDEWWRNEQ
ZmCesA8     (890)  CLLTGKFITPELTNVASIWFMALFICISVTGILEMRWSGVCIDDWWRNEQ
ZmCesA7     (882)  CLLTGKFITPELNNVASLWFMSLFICIFAISILEMRWSGVCIDDWWRNEQ
ZmCesA6     (855)  CLLTGKFITPELNNVASLWFMSLFICIFAISILEMRWSGVGIDDWWRNEQ
ZmCesA5     (872)  CLLTGKFIIPKISNLESVWRISLFISIFATGILEMRWSGVGIDEWWRNEQ
ZmCesA4     (873)  CLLTCKFIIPEISNFASIWFISLFISIFATGILEMRWSGVGIDEWWRNEQ
ZmCesA3     (616)  CLLTNKFIIPAISNYAGAFFILLFASIFATGILELRWSGVGIEDWWRNEQ
ZmCesA2     (869)  CLLTNKFIIPEISNYAGMFFILLFASIFATGILELRWSGVGIEDWWRNEQ
SeqIdNo.30  (847)  CLLTGKFIMPSISTFASLFFIALFMSIFATGILEMRWSGVSIEEWWRNEQ
ZmCesA12    (722)  CLLTGKFIMPSISTFASLFFIALFMSIFATGILEMRWSGVGIEDWWRNEQ
ZmCesA11    (779)  CLLTGKFIIPTLSNAATIWFLGLFMSIIVTSVLELRWSGVSIEDWWRNEQ
ZmCesA10    (873)  CLLTNKFIIPTLNNLASIWFTALFLSBIAISVLELRWSGVGIEDWWRNEQ
ZmCesA1     (870)  CLLTNKFIIPEISNYAGMFFILLFASIFATGILELRWSGVGIEDWWRNEQ
Consensus   (951)  CLLTGKFIIPEISNFASIWFISLFISIFATGILEMRWSGVGIEDWWRNEQ
                   1001                                             1050
ZmCesA9     (925)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFTVTSKAS-DEDGDFAELYMFK
ZmCesA8     (940)  FWVIGGVSAHLFAVFQGLLKVFAGIDTSFTVTSKAG--DDEBFSELYTFK
ZmCesA7     (932)  FWVIGGVSSHLFAVFQGLLKVIAGVDFSFTVTSKGG--DDEBFSELYTFK
ZmCesA6     (905)  FWVIGGVSSHLFAVFQGLLKVIAGVDFSFTVTSKGG--DDEBFSELYTFK
ZmCesA5     (922)  FWVIGGISAHLFAVFQGLLKVLAGIDTSFTVTSKAT-DEBGDFAELYMFK
ZmCesA4     (923)  FWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKAT-DDDGDFAELYVFK
ZmCesA3     (666)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFTVTSKAS-DEDGDFAELYVFK
ZmCesA2     (919)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFTVTSKATGDEDDEFAELYAFK
SeqIdNo.30  (897)  FWVIGGVSAHLFAVVQGLLKVLAGIDTNFTVTSKATGDEDDEFAELYAFK
ZmCesA12    (772)  FWVIGGVSAHLFAVVQGLLKVLAGIDTNFTVTSKATGDEDDEFAELYAFK
ZmCesA11    (829)  FWVIGGVSAHLFAVFQGILKMIAGIDTNFTVTAKAT--DDTEFGELYLFK
ZmCesA10    (923)  FWVIGGVSAHLFAVFQGFLKVLGGVDTSFTVTSKAAGDEADAFGDLVLFK
ZmCesA1     (920)  FWVIGGTSAHLFAVFQGLLKVLAGIDTNFTVTSKAS-DEDGDFAELYVFK
Consensus   (1001) FWVIGGVSAHLFAVFQGLLKVLAGIDTNFTVTSKAT DED DFAELYMFK
                   1051                                             1100
ZmCesA9     (974)  WTTLLIPPTTILILNLVGVVAGISYBINSGYOSWGPLFGKLFFAFWVIVH
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Serial No. 10/627,132
Amendment Dated June 10, 2005
Reply to Office Action of March 11, 2005

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ZmCesA8     (988)  WTTLLIPPTTLLLLNFIGVVAGISNAINNGYESWGPLFGKLFFAFWVIVH
ZmCesA7     (980)  WTTLLIPPTTLLLLNFIGVVAGVSNAINNGYESWGPLFGKLFFAFWVIVH
ZmCesA6     (953)  WTTLLIPPTTELLLNFIGVVAGISNAINNGYESWGPLFGKLFFAFWVIVH
ZmCesA5     (971)  WTTLLIPPTTILTINLVGVVAGISYAINSGYQSWGPLFGKLFFAFWVIVH
ZmCesA4     (972)  WTTLLIPPTTILIINLVGVVAGISYAINSGYQSWGPLFGKLFFAIWVILH
ZmCesA3     (715)  WTTLLTPPTTVLVINLVGIVAGVSYAINSGYQSWGPLFGKLFFSIWVILH
ZmCesA2     (968)  WTSLLIPPTTVLVINLVGMVAGISYAINSGYQSWGPLFGKLFFAFWVIVH
SeqIdNo.30  (947)  WTTLLIPPTTLLIINVIGVVAGISDAINNGYQSWGPLFGKLFFAFWVIVH
ZmCesA12    (822)  WTTLLIPPTTLLIINVIGVVAGISDAINNGYQSWGPLFGKLFFAFWVIVH
ZmCesA11    (877)  WTTVLIPPTSILVINLVGVVAGFSAALNSGYESWGPLFGRVFFAMWVIMH
ZmCesA10    (973)  WTTLLVPPTTLIIINMVGIVAGVSDAVNNGYGSWGPLFGKLFFSFWVIVH
ZmCesA1     (969)  WTSLLIPPTTVLVINLVGMVAGISYAINSGYQSWGPLFGKLFFSIWVILH
Consensus  (1051)  WTTLLIPPTTLLIINLVGVVAGIS AINSGYQSWGPLFGKLFFAFWVIVH
                   1101                                          1150
ZmCesA9    (1024)  LYPFLKGLMGRQNRTPTIVVVWAILLASIFSLLWVRIDPFTNRVTCPD--
ZmCesA8    (1038)  LYPFLKGLVGRQNRTPTIVIVWSILLASIFSLLWVRVDPFLAKSNGPL--
ZmCesA7    (1030)  LYPFLKGLVGRQNRTPTIVIVWSILLASIFSLLWVRIDPFLAKDDGPL--
ZmCesA6    (1003)  LYPFLKGLVGRQNRTPTIVIVWSILLASIFSLLWVRIDPFLAKDDGPL--
ZmCesA5    (1021)  LYPFLKGLMGKQNRTPTIVVVWAILLASIFSLMWVRIDPFTTRVTGPD--
ZmCesA4    (1022)  LYPFLKGLMGRQNRTPTIVVVWAILLASIFSLLWVRIDPFTTRVTGPD--
ZmCesA3     (765)  LYPFLKGLMGKQNRTPTIVIVWSVLLASIFSLLWVKIDPFISPTQKALS-
ZmCesA2    (1018)  LYPFLKGLMGRQNRTPTIVIVWSILLASIFSLLWVKIDPFISPTQKAAA-
SeqIdNo.30  (997)  LYPFLKGLMGRQNRTPTVVVVWSILLASIFSLLWVRIDPFIVRTKGPD--
ZmCesA12    (872)  LYPFLKGLMGRQNRTPTVVVIWSILLASVFSLLWVKIDPFVGGTETVNTN
ZmCesA11    (927)  LYPFLKGLMGRQNRTPTIVVLWSILLASIFSDVWVRIDPFIPKAKGPI--
ZmCesA10   (1023)  LYPFLKGLMGRQNRTPTIVIVWSILLASIFSLLWVKIDPFISPTQKAAA-
ZmCesA1    (1019)  LYPFLKGLMGRQNRTPTIVIVWSILLASIFSLLWVRIDPFI RT GP
Consensus  (1101)  LYPFLKGLMGRQNRTPTIVVVWSILLASIFSLLWVRIDPFI RT GP
                   1151                        1181
ZmCesA9    (1072)  -----------------------TRTCGING------
ZmCesA8    (1086)  -----------------------LEECCLDCN-----
ZmCesA7    (1078)  -----------------------LEECGLDCN-----
ZmCesA6    (1051)  -----------------------LEECGLDCN-----
ZmCesA5    (1069)  -----------------------IAKCGING------
ZmCesA4    (1070)  -----------------------TQTCGING------
ZmCesA3     (814)  -----------------------RGQCGVNC------
ZmCesA2    (1067)  -----------------------IGQCGVNC------
SeqIdNo.30 (1045)  -----------------------VRQCGING------
ZmCesA12    (920)  -----------------------VRQCGINC------
ZmCesA11    (977)  NCNTHLLIHHRSAAVVPRRTCPWCCKRGLPA
ZmCesA10   (1071)  -----------------------EKPCGVEC------
ZmCesA1    (1068)  -----------------------LGQCGVNC------
Consensus  (1151)                          L  CGINC
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Page 25 of 25